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 RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/067,482

 DATE: 03/05/2002  
 TIME: 10:58:40

 Input Set : A:\1U 102 R1.ST25.txt  
 Output Set: N:\CRF3\03052002\J067482.raw

2/25

3 <110> APPLICANT: OriGene Technologies, Inc.  
 5 <120> TITLE OF INVENTION: Angiogenesis Dehydrogenase Gene  
 7 <130> FILE REFERENCE: 1U 102 R1  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/067,482  
 C--> 9 <141> CURRENT FILING DATE: 2002-02-07  
 9 <160> NUMBER/OF SEQ ID NOS: 4  
 11 <170> SOFTWARE: PatentIn version 3.1  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 3727  
 15 <212> TYPE: DNA  
 16 <213> ORGANISM: homo sapiens  
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 19 <221> NAME/KEY: CDS  
 20 <222> LOCATION: (28)..(1689)  
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 26 Met Ala Ala Val Ser Leu Arg Leu Gly  
 27 1 5  
 29 gac ttg gtg tgg ggg aaa ctc ggc cga tat cct cct tgg cca gga aag 102  
 30 Asp Leu Val Trp Gly Lys Leu Gly Arg Tyr Pro Pro Trp Pro Gly Lys  
 31 10 15 20 25  
 33 att gtt aat cca cca aag gac ttg aag aaa cct cgc gga aag aaa tgc 150  
 34 Ile Val Asn Pro Pro Lys Asp Leu Lys Lys Pro Arg Gly Lys Lys Cys  
 35 30 35 40  
 37 ttc ttt gtg aaa ttt ttt gga aca gaa gat cat gcc tgg atc aaa gtg 198  
 38 Phe Phe Val Lys Phe Phe Gly Thr Glu Asp His Ala Trp Ile Lys Val  
 39 45 50 55  
 41 gaa cag ctg aag cca tat cat gct cat aaa gag gaa atg ata aaa att 246  
 42 Glu Gln Leu Lys Pro Tyr His Ala His Lys Glu Glu Met Ile Lys Ile  
 43 60 65 70  
 45 aac aag ggt aaa cga ttc cag caa gcg gta gat gct gtc gaa gag ttc 294  
 46 Asn Lys Gly Lys Arg Phe Gln Gln Ala Val Asp Ala Val Glu Glu Phe  
 47 75 80 85  
 49 ctc agg aga gcc aaa ggg aaa gac cag acg tca tcc cac aat tct tct 342  
 50 Leu Arg Arg Ala Lys Gly Lys Asp Gln Thr Ser Ser His Asn Ser Ser  
 51 90 95 100 105  
 53 gat gac aag aat cga cgt aat tcc agt gag gag aga agt agg cca aac 390  
 54 Asp Asp Lys Asn Arg Arg Asn Ser Ser Glu Arg Ser Arg Pro Asn  
 55 110 115 120  
 57 tca ggt gat gag aag cgc aaa ctt agc ctg tct gaa ggg aag gtg aag 438  
 58 Ser Gly Asp Glu Lys Arg Lys Leu Ser Leu Ser Gly Gly Lys Val Lys  
 59 125 130 135

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61	aag aac atg gga gaa gga aag aag agg gtg tct tca ggc tct tca gag	486
62	Lys Asn Met Gly Glu Gly Lys Lys Arg Val Ser Ser Gly Ser Ser Glu	
63	140 145 150	
65	aga ggc tcc aaa tcc cct ctg aaa aga gcc caa gag caa agt ccc cgg	534
66	Arg Gly Ser Lys Ser Pro Leu Lys Arg Ala Gln Glu Gln Ser Pro Arg	
67	155 160 165	
69	aag cgg ggt cgg ccc cca aag gat gag aag gat ctc acc atc ccg gag	582
70	Lys Arg Gly Arg Pro Pro Lys Asp Glu Lys Asp Leu Thr Ile Pro Glu	
71	170 175 180 185	
73	tct agt acc gtg aag ggg atg atg gcc gga ccg atg gcc gcg ttt aaa	630
74	Ser Ser Thr Val Lys Gly Met Met Ala Gly Pro Met Ala Ala Phe Lys	
75	190 195 200	
77	tgg cag cca acc gca agc gag cct gtt aaa gat gca gat cct cat ttc	678
78	Trp Gln Pro Thr Ala Ser Glu Pro Val Lys Asp Ala Asp Pro His Phe	
79	205 210 215	
81	cat cat ttc ctg cta agc caa aca gag aag cca gct gtc tgt tac cag	726
82	His His Phe Leu Leu Ser Gln Thr Glu Lys Pro Ala Val Cys Tyr Gln	
83	220 225 230	
85	gca atc acg aag aag ttg aaa ata tgt gaa gag gaa act ggc tcc acc	774
86	Ala Ile Thr Lys Lys Leu Lys Ile Cys Glu Glu Glu Thr Gly Ser Thr	
87	235 240 245	
89	tcc atc cag gca gct gac agc aca gcc gtg aat ggc agc atc aca ccc	822
90	Ser Ile Gln Ala Ala Asp Ser Thr Ala Val Asn Gly Ser Ile Thr Pro	
91	250 255 260 265	
93	aca gac aaa aag ata gga ttt ttg ggc ctt ggt ctc atg gga agt gga	870
94	Thr Asp Lys Lys Ile Gly Phe Leu Gly Leu Gly Leu Met Gly Ser Gly	
95	270 275 280	
97	atc gtc tcc aac ttg cta aaa atg ggt cac aca gtg act gtc tgg aac	918
98	Ile Val Ser Asn Leu Leu Lys Met Gly His Thr Val Thr Val Trp Asn	
99	285 290 295	
101	cgc act gca gag aaa tgt gat ttg ttc atc cag gag ggg gcc cgt ctg	966
102	Arg Thr Ala Glu Lys Cys Asp Leu Phe Ile Gln Glu Gly Ala Arg Leu	
103	300 305 310	
105	gga aga acc ccc gct gaa gtc gtc tca acc tgc gac atc act ttc gcc	1014
106	Gly Arg Thr Pro Ala Glu Val Val Ser Thr Cys Asp Ile Thr Phe Ala	
107	315 320 325	
109	tgc gtg tcg gat ccc aag gcg gcc aag gac ctg gtg ctg ggc ccc agt	1062
110	Cys Val Ser Asp Pro Lys Ala Ala Lys Asp Leu Val Leu Gly Pro Ser	
111	330 335 340 345	
113	ggt gtg ctg caa ggg atc cgc cct ggg aag tgc tac gtg gac atg tca	1110
114	Gly Val Leu Gln Gly Ile Arg Pro Gly Lys Cys Tyr Val Asp Met Ser	
115	350 355 360	
117	aca gtg gac gct gac acc gtc act gag ctg gcc cag gtg att gtg tcc	1158
118	Thr Val Asp Ala Asp Thr Val Thr Glu Leu Ala Gln Val Ile Val Ser	
119	365 370 375	
121	agg ggg ggg cgc ttt ctg gaa gcc ccc gtc tca ggg aat cag cag ctg	1206
122	Arg Gly Gly Arg Phe Leu Glu Ala Pro Val Ser Gly Asn Gln Gln Leu	
123	380 385 390	
125	tct aat gac ggg atg ttg gtg atc tta gcg gct gga gac agg ggc tta	1254

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126 Ser Asn Asp Gly Met Leu Val Ile Leu Ala Ala Gly Asp Arg Gly Leu
127      395                      400                      405
129 tat gag gac tgc agc agc tgc ttc cag gcg atg ggg aag acc tcc ttc      1302
130 Tyr Glu Asp Cys Ser Ser Cys Phe Gln Ala Met Gly Lys Thr Ser Phe
131 410                      415                      420                      425
133 ttc cta ggt gaa gtg ggc aat gca gcc aag atg atg ctg atc gtg aac      1350
134 Phe Leu Gly Glu Val Gly Asn Ala Ala Lys Met Met Leu Ile Val Asn
135      430                      435                      440
137 atg gtc caa ggg agc ttc atg gcc act att gcc gag ggg ctg acc ctg      1398
138 Met Val Gln Gly Ser Phe Met Ala Thr Ile Ala Glu Gly Leu Thr Leu
139      445                      450                      455
141 gcc cac gtg aca ggc cag tcc cag cag aca ctc ttg gac atc ctc aat      1446
142 Ala His Val Thr Gly Gln Ser Gln Gln Thr Leu Leu Asp Ile Leu Asn
143      460                      465                      470
145 cag gga cag ttg gcc agc atc ttc ctg gac cag aag tgc caa aat atc      1494
146 Gln Gly Gln Leu Ala Ser Ile Phe Leu Asp Gln Lys Cys Gln Asn Ile
147      475                      480                      485
149 ctg caa gga aac ttt aag cct gat ttc tac ctg aaa tac att cag aag      1542
150 Leu Gln Gly Asn Phe Lys Pro Asp Phe Tyr Leu Lys Tyr Ile Gln Lys
151 490                      495                      500                      505
153 gat ctc cgc tta gcc att gcg ctg ggt gat gcg gtc aac cat ccg act      1590
154 Asp Leu Arg Leu Ala Ile Ala Leu Gly Asp Ala Val Asn His Pro Thr
155      510                      515                      520
157 ccc atg gca gct gca gca aat gag gtg tac aaa aga gcc aag gcg ctg      1638
158 Pro Met Ala Ala Ala Ala Asn Glu Val Tyr Lys Arg Ala Lys Ala Leu
159      525                      530                      535
161 gac cag tcc gac aac gat atg tcc gcc gtg tac cga gcc tac ata cac      1686
162 Asp Gln Ser Asp Asn Asp Met Ser Ala Val Tyr Arg Ala Tyr Ile His
163      540                      545                      550
165 taa gctgtcgaca ccccgccctc acccctccaa tccccctct gacccctct      1739
167 tcctcacatg gggtcggggg cctgggagtt cattctggac cagccacct atctccattt      1799
169 ccttttatac agactttgag acttgccatc agcacagcac acagcagcac ccttcccctg      1859
171 aggccggtgg ggaggggaca agtgtcagca ggattggcgt gtgggaaagc tcttgagctg      1919
173 ggcaactggcc ccccgacga ggtggctgtg tggtcacaca cacacacaca cacacacaca      1979
175 ggctctcgcc ccaggataga agctgcccag aaactgctgc ctggcttttt ttcttccgag      2039
177 cttgtcttat ctcaaaccct ttccagtcaa ggaactagaa tcagcaacga gagttggaag      2099
179 ccttcccaca gcttccccca gagcgaagag gctgtagtca tgtccccatc cccactgga      2159
181 ttccctacaa ggagagggcct tggggccaga tgagccagta cagactccag acagaggggc      2219
183 ccttgggggcc ctccaacctc aggtgatgag ctgagaaaaga tgttcacgtc taagcgtcca      2279
185 gtgtgcaccc agcgtccat agacgccttt gtgaactgaa aagagactgg cagagtcccg      2339
187 agaagatggg gccctggctt tccaggaggat gcagcaagca gccggcctgc aggtgagcat      2399
189 ggaggcccgg ccctcaccgc ctgcaagcca tgccccagat gccactgcca cagcgggcgc      2459
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195 cgtaggcca cagactcttc acctggtct gaagagccac tcttacctcg gtcccctcc      2639
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199 cctccctcct ctccctcttc ctcccgtgga gacagtattt cttctgtct gtcccttg      2759
201 cccagaccca gcctgaccaa cgatgagcat ttcttaggct cagctcttga tacggaaacg      2819
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205 ggaggggaaga gaactgggcc tgacctacct gaactgactg gccctccgag gtgggtctgg 2939
207 gacatcctag aggccctaca tttgtccttg gatagggggac cgggggggggc ttggaatgtt 2999
209 gcaaaaaaaaa aagttaccca agggatgtca gttttttatc cctctgcatg ggttggattt 3059
211 tccaaaatca taatttgcag aaggaaggcc agcatttatg atgcaatatg taattatata 3119
213 taggggtggcc acactagggc ggggtccttc cccctcaca gctttggccc ctttcagaga 3179
215 ttagaaaactg ggtagagga ttgcagaaga cgagtggggg gagggcaggg aagatgcctg 3239
217 tcgggttttt agcacagttc atttcaactg gattttgaag ctttctgtc tgaacacaaa 3299
219 gcctgttcta gtcctggcgg aacacactgg ggggtggggc gggggaagat gcggtaatga 3359
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225 gtgacacttg tgaaaaagct tgtaagaaag cccctccctt tttcttttaa acctttaaat 3539
227 gacaaatcta ggtaatgaag gttgtgaatt tttatttttg ctttgttttt aatgaacatt 3599
229 tgtctttcag aataggattg tgtgataatg tttaaatggc aaaaacaaaa catgattttg 3659
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237 <211> LENGTH: 553
238 <212> TYPE: PRT
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247 Gly Arg Tyr Pro Pro Trp Pro Gly Lys Ile Val Asn Pro Pro Lys Asp
248 20 25 30
251 Leu Lys Lys Pro Arg Gly Lys Lys Cys Phe Phe Val Lys Phe Phe Gly
252 35 40 45
255 Thr Glu Asp His Ala Trp Ile Lys Val Glu Gln Leu Lys Pro Tyr His
256 50 55 60
259 Ala His Lys Glu Glu Met Ile Lys Ile Asn Lys Gly Lys Arg Phe Gln
260 65 70 75 80
263 Gln Ala Val Asp Ala Val Glu Glu Phe Leu Arg Arg Ala Lys Gly Lys
264 85 90 95
267 Asp Gln Thr Ser Ser His Asn Ser Ser Asp Asp Lys Asn Arg Arg Asn
268 100 105 110
271 Ser Ser Glu Glu Arg Ser Arg Pro Asn Ser Gly Asp Glu Lys Arg Lys
272 115 120 125
275 Leu Ser Leu Ser Glu Gly Lys Val Lys Lys Asn Met Gly Glu Gly Lys
276 130 135 140
279 Lys Arg Val Ser Ser Gly Ser Ser Glu Arg Gly Ser Lys Ser Pro Leu
280 145 150 155 160
283 Lys Arg Ala Gln Glu Gln Ser Pro Arg Lys Arg Gly Arg Pro Pro Lys
284 165 170 175
287 Asp Glu Lys Asp Leu Thr Ile Pro Glu Ser Ser Thr Val Lys Gly Met
288 180 185 190
291 Met Ala Gly Pro Met Ala Ala Phe Lys Trp Gln Pro Thr Ala Ser Glu
292 195 200 205
295 Pro Val Lys Asp Ala Asp Pro His Phe His His Phe Leu Leu Ser Gln
296 210 215 220
299 Thr Glu Lys Pro Ala Val Cys Tyr Gln Ala Ile Thr Lys Lys Leu Lys

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303 Ile Cys Glu Glu Glu Thr Gly Ser Thr Ser Ile Gln Ala Ala Asp Ser
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308          260          265          270
311 Leu Gly Leu Gly Leu Met Gly Ser Gly Ile Val Ser Asn Leu Leu Lys
312          275          280          285
315 Met Gly His Thr Val Thr Val Trp Asn Arg Thr Ala Glu Lys Cys Asp
316          290          295          300
319 Leu Phe Ile Gln Glu Gly Ala Arg Leu Gly Arg Thr Pro Ala Glu Val
320 305          310          315          320
323 Val Ser Thr Cys Asp Ile Thr Phe Ala Cys Val Ser Asp Pro Lys Ala
324          325          330          335
327 Ala Lys Asp Leu Val Leu Gly Pro Ser Gly Val Leu Gln Gly Ile Arg
328          340          345          350
331 Pro Gly Lys Cys Tyr Val Asp Met Ser Thr Val Asp Ala Asp Thr Val
332          355          360          365
335 Thr Glu Leu Ala Gln Val Ile Val Ser Arg Gly Gly Arg Phe Leu Glu
336          370          375          380
339 Ala Pro Val Ser Gly Asn Gln Gln Leu Ser Asn Asp Gly Met Leu Val
340 385          390          395          400
343 Ile Leu Ala Ala Gly Asp Arg Gly Leu Tyr Glu Asp Cys Ser Ser Cys
344          405          410          415
347 Phe Gln Ala Met Gly Lys Thr Ser Phe Phe Leu Gly Glu Val Gly Asn
348          420          425          430
351 Ala Ala Lys Met Met Leu Ile Val Asn Met Val Gln Gly Ser Phe Met
352          435          440          445
355 Ala Thr Ile Ala Glu Gly Leu Thr Leu Ala His Val Thr Gly Gln Ser
356          450          455          460
359 Gln Gln Thr Leu Leu Asp Ile Leu Asn Gln Gly Gln Leu Ala Ser Ile
360 465          470          475          480
363 Phe Leu Asp Gln Lys Cys Gln Asn Ile Leu Gln Gly Asn Phe Lys Pro
364          485          490          495
367 Asp Phe Tyr Leu Lys Tyr Ile Gln Lys Asp Leu Arg Leu Ala Ile Ala
368          500          505          510
371 Leu Gly Asp Ala Val Asn His Pro Thr Pro Met Ala Ala Ala Ala Asn
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376          530          535          540
379 Ser Ala Val Tyr Arg Ala Tyr Ile His
380 545          550
383 <210> SEQ ID NO: 3
384 <211> LENGTH: 547
385 <212> TYPE: PRT
386 <213> ORGANISM: homo sapiens
388 <400> SEQUENCE: 3
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VERIFICATION SUMMARY

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Input Set : A:\1U 102 R1.ST25.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date